

QY 660 TGTTCAAAGGAAATTGACAAATGGCCCTCCCAACTCTGTATCCATTACCTTCACG 719
 Db 259 TGTTCAAAGGAAATTGACAAATGGCCCTCCCAACTCTGTATCCATTACCTTCACG 200
 QY 720 TCCACCGATGCTATTCTAGACATCATCAGTGGATAACAGTGTATGGTTGTTACA 779
 Db 199 TCCACCGATGCTATTCTAGACATCATCAGTGGATAACAGTGTATGGTTGTTACA 140
 QY 780 TGAATGTTGTTTACTGTAGGAGTTGATTTAGTAAAGTGTCT 839
 Db 139 TGAATGTTGTTTACTGTAGGAGTTGATTTAGTAAAGTGTCT 80
 QY 840 AAAAAGGGGACAGAGAACTATAAGGCAACTATAAGGCAACTATAAGGCAATGTA 894
 Db 79 AAAAAGGGGACAGAGAACTATAAGGCAACTATAAGGCAATGTA 25

RESULT 3
 LOCUS BM2/205/c. 621 bp mRNA linear EST 20-DEC-2001
 DEFINITION Ig38e04_Y1 HR85 islet Homo sapiens cDNA 5' similar to TR.Q9TJK0

ACCESSION BM2/2057
 VERSION GI:17965335

KEYWORDS EST

ORGANISM Homo sapiens (human)

Bukaryote; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE (bases: 1 to 621)
 Maton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Scraer, M., Brestelli, J., Gradwohl, G., Clifton, S., Lemishka, I., Marra, M., Pape, D., Wyllie, T., Martin, J., Blitsain, A., Hillier, L., Theising, B., Ritter, E., Ronk, I., Bennett, J., Cardenas, Schmitz, A., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium
 Unpublished

Other ESTs: 1938e04_x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812
 Fax: 617-495-6557

Email: dmelton@biophys.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)
 Possible reversed clone: Similarity on wrong strand
 Seq primer: -40P from Gibson
 High quality sequence stop: 116.

Location Qualifiers
 1. .621

organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 tissue_type="Purified pancreatic islet"
 /lb_host="DH10B"
 /clone_lib="HR85 islet"

/note="Organ: Pancreas; Vector: Bluscript SK(-); Site_1: Not1; Site_2: XbaI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XbaI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@im.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

FEATURES source
 RESULT 4
 AA625895/c
 LOCUS AA625895
 DEFINITION zuera10_s1.Scaries_testis_NHT Homo sapiens mRNA
 3' mRNA sequence.

ACCESSION AA625895
 VERSION AA625895.1
 KEYWORDS EST
 SOURCE Homo sapiens (Human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 475)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geissel, G., Jost, S., Kizman, D., Kuchaba, T., Lacy, M., Le, N., Lemmon, G., Marr, M., Martin, J., Moore, B., Scheibenbogen, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE Wash-NCI Human EST Project

BASE COUNT 163 a 120 c 123 g 215 t

TITLE Direct Submission (16-JUN-1999) Hiroshi Gomi, The Institute of Physical and Chemical Research (RIKEN), Brain Science Institute (BSI); 2-1
JOURNAL Submitted
Author Hiroshi Gomi, Wako, Saitama 351-0138, Japan
 (E-mail: hgomi@brain.riken.go.jp, Tel.:+81-48-467-9724,
 Fax: +81-48-467-9725)

FEATURES

source	Location/Qualifiers	Value		
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	/mol type="mRNA"			
	/db_xref="taxon:9986"			
	/sex="male"			
	/issue type="brain"			
2	2022	"Note: corresponds to mouse KKIARE-beta"		
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	/product="Ser/Thr kinase KKIARE"			
	/protein id="P0AA86508_1"			
	/db_xref="GI_64427"			
	/translation="MEK1YENLKLKORHENLVNLLEVCCKKCNMGRSGRFAIKRFLLESSDDKRMV KKIANRENLKLKORHENLVNLLEVCCKKCNMGRSGRFAIKRFLLESSDDKRMV VOKYLQOLLGICHSNHLIRDEKPIENLNSQSOVYKLCDFEPARTLAAPEPVYTD YNATWYRQAFPLNLLGVKGRADWVAGLTMEMGPEVPLGDSIDQNLJMRCL GNLPIAELHDFDNDKGEAFRFSQLOVKQDNRNLKATYMSMWTGSPHJKAVASITSRL KTLVYQDNTNSKDKSVPKIGSKDGEKWDKNTENLKATYMSMWTGSPHJKAVASITSRL DCSNVSDETRPAGPMAPIPLHNLSAVPGINSMGMENTPGVOSYRDEKIKCIPFV KPNKGHSPPGSIYNNVNTNTSVESSKRNLLQANKKGEYKRTDYLPELNYNHLPELALEG TARNRSLLRKENKILSLRISPLSLAIDLHTPNUHQVSQSPSLSDGEADSPPMHEQH "			
BASE COUNT	939 a	577 c	777 g	860 t
ORIGIN				

Query Match Score 620.6; Dp 4; Length 3153;
Best Local Similarity 37.4%; **Pred.** No. 3.5e/141; **Indels** 16;
Matches 1003; **Conservative** 0; **Mismatches** 229;

Query	Start	End	Score	Length
1	2	61	1541	1600
2	62	121	1601	1657
3	122	181	1638	1717
4	182	240	1778	1837
5	1777	2041	1838	1897
6	207	361	1898	420
7	207	481	1958	500
8	207	2018	2018	598

Query Match Score 620.6; Dp 4; Length 3153;
Best Local Similarity 76.7%; **Pred.** No. 3.5e/141; **Indels** 16;
Matches 1003; **Conservative** 0; **Mismatches** 229;

Query	Start	End	Score	Length
1	2	61	1541	1600
2	62	121	1601	1657
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5	1777	2041	1838	1897
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8	207	2018	2018	598

Query Match Score 620.6; Dp 4; Length 3153;
Best Local Similarity 76.7%; **Pred.** No. 3.5e/141; **Indels** 16;
Matches 1003; **Conservative** 0; **Mismatches** 229;

Query	Start	End	Score	Length
1	2	61	1541	1600
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3	122	181	1638	1717
4	182	240	1778	1837
5	1777	2041	1838	1897
6	207	361	1898	420
7	207	481	1958	500
8	207	2018	2018	598

RESULT 4
 AR221994
LOCUS 3080 bp DNA
DEFINITION Sequence 3 from patent US 6728937.
ACCESSION AR221994
VERSION 1
KEYWORDS Unknown
SOURCE Unclassified.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3080)
AUTHORS Thompson, R. F., Gomi, H. and Sun, W.
TITLE CDNA, genomic, and predicted protein sequences of learning-induced kinases
JOURNAL Patent: US 6426994-A 3 06-Aug-2002;
FEATURES Location/Qualifiers
 1. 3080 /organism="unknown"
BASE COUNT 930 a 556 c 751 g 843 t
ORIGIN

Query Match	37.1%	Score	624.8	DB	6	Length	3080	;
Best Local Similarity	76.5%	Pred.	No. 5-140;					
Matches 1000;	Conservative	0;	Mismatches	232;	Indels	76;	Gaps	16;
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1468	TGCCCCATTCCCCCTTACATCTGGAGTTGCTCCAGCATTAATCTGGAA	1527						
62	TGGGACTGAGACTTACACATTAGGGTACAGTGATGAGAAAATAGAGTGT	121						
1528	TGGGACT - ATCCGAGCTGAGTTACAGTGATGAGAAAATAGAGTGT	1584						
122	CTATTCATTGTGAAACCGAACAGACATCCCATGAGCATTATAACATTAAATGTGA	181						
1585	GTATTCATTGTGAAACCTTCCATTCAACATCTCCATTATAATGTGA	1644						
182	CCACATTACTCTCTAGTAAGAAAGAGAAATCT	240						
1645	CCACATCGTCTCCAGTGAAGAACCTTCCAGCAAAACAGAAAGGGAGACT	1704						
241	CCAGGAGAGATGRCGTTGCCNTAACTATAATCTCCCTGACTTAAGAGCAC	300						
1705	CCAGACAGATGCGTTGCCNTAACTATAATCTCCCTGACTTAAGAGCT	1764						
301	TGGAGGGATAGCTGAAATTCCAGGTTAACAAAGAAAGGAAAATTCTTCAGAT	360						
1765	TGAAGGGATGCTGAAATTAGGCTTACAGTCATTAAGGAAATACTTCAGAT	1824						
361	CTGCAGATCTCTCTGCTGCTGCTATTGACTGCAACCCCGATTAAGCTTACAG	420						
1825	CTGAAATTCCCTCTGGTGCCTTACAGTCATGACACACCAAAATTCAGG	1884						
421	TATCGGACTCTCCCTGTAAAGTATCAGGGCTGATTTGCCTCAAATGAAAC	480						
1895	TGTGAGGATCTCCCTGCTGAGCTTCAAGGGCTGTTGGCTGGAGAACGCC	1944						
481	ACTGAGAACCTTT-TGGTCTGAACTGGATGATGCTGACTCTGGATGACATCT	538						
1945	ACTGAAGATCACTGGTGTCTGATCGATGCTGGATGGACCTCT	2004						
539	CTTGAGGAGAGCTGCTGATATCCAAAGAGGATTTGCACTTCCCTC	598						
2005	CTCCAAACAAAGCTGCTGATATCCTAGGAGATGGCTTGGGTGTCCTC	2064						
599	TGACTGCCTGATTTCTGAGGAGGCTCTAGAAGGAAAGACAAGACTCCAA	658						
2065	TGACTGCCTGATTTCTGAGGAGGCTCTAGAAGGAAAGACAAGACTCCAA	2124						
659	ATCTTCAAAGGAGATGAAACAAATGGCCTCCCAACTGTTACCTCCATAC	718						
2125	ATGTTCAAAGAGATTCACAGTACTCCATACAGTACTCCATAC	2183						
719	GTGCCAGCATGCTTACAGTACATGCTGAAATACAGTATGGTCTGGTAC	778						
2184	GTCCACTGCTGATTCAGATCTCAAGTCTCA - GAAAGAGGGTGTAC	2241						
779	ATGATGTTGATTTACTGTTAGGATGTTGATTTAAAGCTT - CCATGATTTAAAGCT	837						
2242	ATGATGTTGATTTACTGTTAGGATGTTGATTTAAAGCTT - CCATGATTTAAAGCT	2301						
838	GTAAAAGGGGACAGAGAAATACTATAAGCCATGTTACTCATGCTGAACTT	897						
2302	GTCAGAAGAG-----AGAGATGATTCACAAATG-----TCATGATGAACTT	2346						
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2347	- TGTGTTATCTGTTAAATGTAAGGATTTATGTTGAGGTTGGGTGTTGTA	2404						
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2405	AGA-----AACTGGGATAGTGTGAAACTAGGAGAAACTGTT	2434						